



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/804,762

DATE: 07/27/2004
TIME: 12:46:57

Input Set : A:\A-72186.ST25.txt
Output Set: N:\CRF4\07272004\J804762.raw

3 <110> APPLICANT: Qi, Yan
4 Zhang, Xianghua
5 Konigsberg, Paula
7 <120> TITLE OF INVENTION: Specific Inhibition of Allorejection
9 <130> FILE REFERENCE: A-72186/TAL/DCF (471702-00005)
11 <140> CURRENT APPLICATION NUMBER: US 10/804,762
12 <141> CURRENT FILING DATE: 2004-03-19
14 <150> PRIOR APPLICATION NUMBER: US 60/456,378
15 <151> PRIOR FILING DATE: 2003-03-19
17 <160> NUMBER OF SEQ ID NOS: 32
19 <170> SOFTWARE: PatentIn version 3.2
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 235
23 <212> TYPE: PRT
24 <213> ORGANISM: Homo sapiens
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33 20 25 30
36 Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser
37 35 40 45
40 Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
41 50 55 60
44 Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
45 65 70 75 80
48 Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
49 85 90 95
52 Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
53 100 105 110
56 Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
57 115 120 125
60 Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg
61 130 135 140
64 Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
65 145 150 155 160
68 Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
69 165 170 175
72 Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
73 180 185 190
76 Cys Gly Val Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His
77 195 200 205
80 Arg Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser

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98	tggccttacc agtgaccgccc ttgctcctgc cgctggcctt gctgctccac gcccggcaggc	180		
100	cgagccagtt ccgggtgtcg cgcgtggatc ggacctggaa cctggggcgag acagtggagc	240		
102	tgaagtgcga ggtgctgctg tccaaaccgaa cgtcgggctg ctcgtggctc ttccagccgc	300		
104	gccccgcgcg cgcagatccc accttccctcc tataacctctc ccaaaaacaag cccaaaggcg	360		
106	ccgaggggct ggacacccag cggttctcggt gcaagagggtt gggggacacc ttgcgtcctca	420		
108	ccctgagcga cttccgcga gagaacgagg gctactatcc ctgctcggcc ctgagcaact	480		
110	ccatcatgtt cttcagccac ttgcgtccgg tcttcctgccc agcgaagccc accacgacgc	540		
112	cagcgcgcg accaccaaca cccggccca ccatcgctc gcagccctg tccctgcgc	600		
114	cagaggcgtg ccggccagcg gcggggggcg cagtgcacac gaggggctg gacttcgcct	660		
116	gtgatatacta catctggcgcc cccttggccgg ggacttgggg ggtccttcctc ctgtcactgg	720		
118	ttatcaccc ttactgcaac cacaggaacc gaagacgtgt ttgcaaatgt ccccgccctg	780		
120	tggtcaatc gggagacaag cccagccctt cggcgagata cgtctaacc ttgcacaacag	840		
122	ccactacatt acttcaaact gagatccctc cttttgaggg agcaagtcc tccctttcat	900		
124	ttttccagt cttccctccct gtgtattcat tctcatgatt attatttttag tggggggcggg	960		
126	gtggaaaga ttacttttc ttatgtgtt tgacggaaa caaaacttagg taaaatctac	1020		
128	agtacaccac aaagggtcaca atactgtgt ggcacatcg cggtaggcg tgaaaagggg	1080		
130	caggccagag ctacccgcag agttctcaga atcatgctga gagagctgga ggcacccatg	1140		
132	ccatctcaac ctctcccccg cccgttttac aaaggggggag gctaaagccc agagacagct	1200		
134	tgatcaaagg cacacagcaa gtcagggttg ggcgttgc tgaggacc ttgtctccca	1260		
136	gctcaggcgct cttccctcca caccattcag gtctttctt ccgaggcccc tgcgtcagg	1320		
138	tgaggtgctt gagtctccaa cggcaaggaa acaagtactt cttgataacct ggatactgt	1380		
140	gcccagagcc tcgaggaggat aatgaattaa agaagagaac tgccttggc agagttctat	1440		
142	aatgtaaaca atatcagact ttttttttataatcaagc cttttttttt atagacctaa	1500		
144	aataaaatga agtggtgagc ttaaccctgg aaaaatgaatc ctttctatctc taaaagaaaat	1560		
146	ctctgtgaaa cccctatgtg gaggcggaat tgctctccca gccccttgc tgcagagggg	1620		
148	cccatgaaag aggacaggct acccccttac aaatagaatt tgagcatcag tgaggtaaa	1680		
150	ctaaggccct cttgaatctc tgaatttgag atacaaacat gttcctggga tcaactgatga	1740		
152	cttttatac tttgtaaaga caattgtgg agagccctc acacaggccct ggcctctgct	1800		
154	caactagcag atacagggt gaggcagacc tgactctctt aaggaggctg agagccaaa	1860		
156	ctgctgtccc aaacatgcac ttccctgctt aaggtatggt acaagcaatg cctgcccatt	1920		
158	ggagagaaaa aacttaagta gataaggaaa taagaaccac tcataattct tcacctttagg	1980		
160	aataatctcc tggtaatatg gtgtacattc ttccctgatta ttttctacac atacatgtaa	2040		
162	aatatgtctt tcttttttaa atagggtgt actatgtgt tatgagtggc tttatgaat	2100		
164	aaacatttgt agcatcctt ttaatggta aacagcaaaa aaaaaaaaaa aaaaaaaaaa	2160		
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171	<210> SEQ ID NO: 3			
172	<211> LENGTH: 198			
173	<212> TYPE: PRT			

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174 <213> ORGANISM: Homo sapiens
 176 <400> SEQUENCE: 3
 178 Met Ala Leu Pro Val Thr Ala Leu Leu Pro Leu Ala Leu Leu Leu
 179 1 5 10 15
 182 His Ala Ala Arg Pro Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr
 183 20 25 30
 186 Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser
 187 35 40 45
 190 Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
 191 50 55 60
 194 Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
 195 65 70 75 80
 198 Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
 199 85 90 95
 202 Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
 203 100 105 110
 206 Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
 207 115 120 125
 210 Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Pro Ala Pro Arg
 211 130 135 140
 214 Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
 215 145 150 155 160
 218 Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Gly Asn Arg Arg Arg
 219 165 170 175
 222 Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser Gly Asp Lys Pro Ser
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 226 Leu Ser Ala Arg Tyr Val
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 231 <211> LENGTH: 2150
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 235 <400> SEQUENCE: 4
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 240 tggccttacc agtgaccgccc ttgctcctgc cgctggcctt gctgctccac gccgcccaggc 180
 242 cgagccagtt ccgggtgtcg ccgctggatc ggacctggaa cctggcgag acagtggagc 240
 244 tgaagtgcaca ggtgctgctg tccaaacccga cgtcgggctg ctcgtgctc ttccagccgc 300
 246 gccgcgcgc cgcaggatccc actttcctcc tatacctctc ccaaaaacaag cccaaggcgg 360
 248 ccgaggggct ggacacccag cggttctcg gcaagagggtt gggggacacc ttctgtcctca 420
 250 ccctgagcga ctccgcga gagaacgagg gctactattt ctgtctggcc ctgagcaact 480
 252 ccatcatgtt cttcagccac ttctgtgcgg tcttcctgcc agcgaagccc accacgacgc 540
 254 cagcgcgcgc accaccaaca ccggcgccca ccatcgccgc gcagccctg tccctgcgc 600
 256 cagaggcgtg ccggccagcg gggggggcg cagggaaaccg aagacgtgtt tgcaaatgtc 660
 258 cccggcctgt ggtcaaatcg ggagacaagc ccagccttgc ggcgagatac gtctaaaccct 720
 260 gtgcaacacgc cactacatta cttcaaaactg agatccttcc ttttggggaa gcaagtccct 780
 262 cccttcatt tttccagtc ttccctccctg tgtatttcatt ctcatgattt ttattttagt 840
 264 gggggcgggg tgggaaagat tacttttct ttatgtgtt gacgggaaac aaaacttaggt 900
 266 aaaatctaca gtacaccaca agggtcacaa tactgttgcg cgcacatcgc ggttagggcgt 960

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268	ggaaaggggc	aggccagagc	tacccgcaga	gttctcagaa	tcatgctgag	agagctggag	1020
270	gcacccatgc	catctcaacc	tcttccccgc	ccgttttaca	aagggggagg	ctaaagccoa	1080
272	gagacagctt	gatcaaaggc	acacagcaag	tcagggttgg	agcagtagct	ggagggacct	1140
274	tgtctccca	ctcagggctc	tttcctccac	accattcagg	tctttcttc	cgaggcccot	1200
276	gtctcaggt	gagggtctg	agtctccaac	ggcaaggaa	caagtacttc	ttgatacctg	1260
278	ggatactgtg	cccagagct	cgaggaggt	atgaattaaa	gaagagaact	gcctttggca	1320
280	gagttctata	atgtaaacaa	tatcagactt	tttttttta	taatcaagcc	taaaattgt	1380
282	tagacctaaa	ataaaaatgaa	gtggtgagct	taaccctgga	aatgaatcc	ctctatctct	1440
284	aaagaaaatc	tctgtgaaac	ccctatgtgg	aggcggatt	gctctccag	cccttgcat	1500
286	gcagaggggc	ccatgaaaga	ggacaggcta	ccccttaca	aatagaattt	gagcatcagt	1560
288	gaggttaaac	taaggccctc	ttgaatctct	gaatttgaga	tacaaacatg	ttcttgggat	1620
290	caactgatgac	tttttatact	ttgtaaagac	aattgttgg	gagcccctca	cacagccctg	1680
292	gcctctgctc	aactagcaga	tacagggatg	aggcagacct	gactctctta	aggaggctga	1740
294	gagcccaaac	tgctgtccca	aacatgcact	tccttgctt	aggtatggta	caagcaatgc	1800
296	ctgcccattg	gagagaaaaa	acttaagttag	ataagggaaat	aagaaccact	cataattctt	1860
298	caccttagga	ataatctcct	gttaatatgg	tgtacattct	tcctgattat	tttctacaca	1920
300	tacatgtaaa	atatgtctt	ctttttaaa	tagggttggta	ctatgctgtt	atgagtggct	1980
302	ttaatgaata	aacatttgt	gcatcctctt	taatggtaa	acagcaaaaa	aaaaaaaaaaa	2040
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310 <211> LENGTH: 198

311 <212> TYPE: PRT

312 <213> ORGANISM: Pongo pygmaeus

314 <400> SEQUENCE: 5

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321							20			25				30		
324	Trp	Asn	Leu	Gly	Glu	Thr	Val	Glu	Leu	Lys	Cys	Gln	Val	Leu	Leu	Ser
325							35			40				45		
328	Asn	Pro	Thr	Ser	Gly	Cys	Ser	Trp	Leu	Phe	Gln	Pro	Arg	Gly	Ala	Ala
329							50			55				60		
332	Ala	Ser	Pro	Thr	Phe	Leu	Leu	Tyr	Leu	Ser	Gln	Asn	Lys	Pro	Lys	Ala
333							65			70				75		
336	Ala	Glu	Gly	Leu	Asp	Thr	Gln	Arg	Phe	Ser	Gly	Lys	Arg	Leu	Gly	Asp
337							85			90				95		
340	Thr	Phe	Val	Leu	Thr	Leu	Ser	Asp	Phe	Arg	Arg	Glu	Asn	Glu	Gly	Tyr
341							100			105				110		
344	Tyr	Phe	Cys	Ser	Ala	Leu	Ser	Asn	Ser	Ile	Met	Tyr	Phe	Ser	His	Phe
345							115			120				125		
348	Val	Pro	Val	Phe	Leu	Pro	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys
349							130			135				140		
352	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu
353							145			150				155		
356	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn	His	Arg	Asn	Arg	Arg	Arg
357							165			170				175		
360	Val	Cys	Lys	Cys	Pro	Arg	Pro	Val	Val	Lys	Ser	Gly	Gly	Lys	Pro	Ser
361							180			185				190		

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368 <210> SEQ ID NO: 6
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370 <212> TYPE: DNA
371 <213> ORGANISM: Pongo pygmaeus
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378 ctgaagtgcc aggtgctgt gtccaaacccg acgtctggct gctcctggct cttccagccg 180
380 cgtggcggccg ccggcagtc cacccttccctc ctatacctct cccaaaacaa gcccaaggcg 240
382 gccgaggggc tggacaccca gcggttctcg ggcaagaggt tgggggacac ctctgtcctc 300
384 accctgagcg acttccgccc ggagaacgaa ggctactatt tctgctcggc cctgagcaac 360
386 tccatcatgt acttcagcca cttcgtgccg gtcttcctgc cagtgcacac gagggggctg 420
388 gacttcgcct gtgatatacta catctggcg cccttggccg ggacctgtgg ggtccttctc 480
390 ctgtcaactgg ttatcaccct ttactgcaac cacaggaacc gaagacgtgt ttgcaaatgt 540
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397 <212> TYPE: PRT
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407 20 25 30
410 Glu Leu Arg Ile Phe Pro Lys Lys Met Asp Ala Glu Leu Gly Gln Lys
411 35 40 45
414 Val Asp Leu Val Cys Glu Val Leu Gly Ser Val Ser Gln Gly Cys Ser
415 50 55 60
418 Trp Leu Phe Gln Asn Ser Ser Lys Leu Pro Gln Pro Thr Phe Val
419 65 70 75 80
422 Val Tyr Met Ala Ser Ser His Asn Lys Ile Thr Trp Asp Glu Lys Leu
423 85 90 95
426 Asn Ser Ser Lys Leu Phe Ser Ala Met Arg Asp Thr Asn Asn Lys Tyr
427 100 105 110
430 Val Leu Thr Leu Asn Lys Phe Ser Lys Glu Asn Glu Gly Tyr Tyr Phe
431 115 120 125
434 Cys Ser Val Ile Ser Asn Ser Val Met Tyr Phe Ser Ser Val Val Pro
435 130 135 140
438 Val Leu Gln Lys Val Asn Ser Thr Thr Lys Pro Val Leu Arg Thr
439 145 150 155 160
442 Pro Ser Pro Val His Pro Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu
443 165 170 175
446 Asp Cys Arg Pro Arg Gly Ser Val Lys Gly Thr Gly Leu Asp Phe Ala
447 180 185 190
450 Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Ile Cys Val Ala Leu
451 195 200 205
454 Leu Leu Ser Leu Ile Ile Thr Leu Ile Cys Tyr His Arg Ser Arg Lys

VERIFICATION SUMMARY

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